

1/13

SEQUENCE LISTING

<110> THE SIR MORTIMER B. DAVIS-JEWISH GENERAL HOSPITAL

<120> HIGHLY ACTIVE FORMS OF INTERFERON REGULATORY FACTOR

PROTEINS

<130> IRF-3

<140>

<141>

<150> CA 2,234,588

<151> 1998-04-07

<160> 11

<170> PatentIn Ver. 2.0

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<212> DNA

<213> Homo sapiens

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<221> CDS

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gac	ctg	ggg	caa	ctg	gag	ggc	gtg	gcc	tgg	gtg	aac	aag	agc	cgc	acg	96
Asp	Leu	Gly	Gln	Leu	Glu	Gly	Val	Ala	Trp	Val	Asn	Lys	Ser	Arg	Thr	
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cgc	ttc	cgc	atc	cct	tgg	aag	cac	ggc	cta	cgg	cag	gat	gca	cag	cag	144
Arg	Phe	Arg	Ile	Pro	Trp	Lys	His	Gly	Leu	Arg	Gln	Asp	Ala	Gln	Gln	
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gag	gat	ttc	gga	atc	ttc	cag	gcc	tgg	gcc	gag	gcc	act	ggt	gca	tat	192
Glu	Asp	Phe	Gly	Ile	Phe	Gln	Ala	Trp	Ala	Glu	Ala	Thr	Gly	Ala	Tyr	
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Val	Pro	Gly	Arg	Asp	Lys	Pro	Asp	Leu	Pro	Thr	Trp	Lys	Arg	Asn	Phe	
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ag	ca	gac	cct	cac	gac	cca	cat	aaa	atc	tac	gag	ttt	gtg	aac	tca		336	
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gga	ggc	agt	act	tct	gat	acc	cag	gaa	gac	att	ctg	gat	gag	tta	ctg		432	
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gac	aat	ccc	act	ccc	ttc	cca	aac	ctg	ggg	ccc	tct	gag	aac	cca	ctg		576	
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Lys	Arg	Leu	Leu	Val	Pro	Gly	Glu	Glu	Trp	Glu	Phe	Glu	Val	Thr	Ala			
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Phe	Tyr	Arg	Gly	Arg	Gln	Val	Phe	Gln	Gln	Thr	Ile	Ser	Cys	Pro	Glu			
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Cys	His	Thr	Tyr	Trp	Ala	Val	Ser	Glu	Glu	Leu	Leu	Pro	Asn	Ser	Gly			
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His	Gly	Pro	Asp	Gly	Glu	Val	Pro	Lys	Asp	Lys	Glu	Gly	Gly	Val	Phe			
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gga	cg	tca	cca	cg	tat	gcc	ctc	tgg	ttc	tgt	gtg	ggg	gag	tca	tgg		1056	
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 ccc acg tgc ctc agg gcc ttg gta gaa atg gcc cgg gta ggg ggt gcc 1152
 Pro Thr Cys Leu Arg Ala Leu Val Glu Met Ala Arg Val Gly Gly Ala
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 Ser Ser Leu Glu Asn Thr Val Asp Leu His Ile Asp Asn Asp His Pro
 385 390 395
 ctc gac ctc gac gac gac cag tac aag gcc tac ctg cag gac ttg gtg 1248
 Leu Asp Leu Asp Asp Asp Gln Tyr Lys Ala Tyr Leu Gln Asp Leu Val
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<213> Homo sapiens

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 35 40 45
 Glu Asp Phe Gly Ile Phe Gln Ala Trp Ala Glu Ala Thr Gly Ala Tyr
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 Val Pro Gly Arg Asp Lys Pro Asp Leu Pro Thr Trp Lys Arg Asn Phe
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 Arg Ser Ala Leu Asn Arg Lys Glu Gly Leu Arg Leu Ala Glu Asp Arg
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 Ser Lys Asp Pro His Asp Pro His Lys Ile Tyr Glu Phe Val Asn Ser
 100 105 110
 Gly Val Gly Asp Phe Ser Gln Pro Asp Thr Ser Pro Asp Thr Asn Gly
 115 120 125
 Gly Gly Ser Thr Ser Asp Thr Gln Glu Asp Ile Leu Asp Glu Leu Leu
 130 135 140
 Gly Asn Met Val Leu Ala Pro Leu Pro Asp Pro Gly Pro Pro Ser Leu
 145 150 155
 Ala Val Ala Pro Glu Pro Cys Pro Gln Pro Leu Arg Ser Pro Ser Leu
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 Asp Asn Pro Thr Pro Phe Pro Asn Leu Gly Pro Ser Glu Asn Pro Leu
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DESIGN

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Trp Leu Leu Gly Glu Ile Ser Ser Gly Cys Tyr Glu Gly Leu Gln Trp	
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Arg Lys Asp Leu Ser Glu Ala Asp Ala Arg Ile Phe Lys Ala Trp Ala	
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Val Ala Arg Gly Arg Trp Pro Pro Ser Ser Arg Gly Gly Gly Pro Pro	
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Pro Glu Ala Glu Thr Ala Glu Arg Ala Gly Trp Lys Thr Asn Phe Arg	
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Cys Ala Leu Arg Ser Thr Arg Arg Phe Val Met Leu Arg Asp Asn Ser	
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Gly Asp Pro Ala Asp Pro His Lys Val Tyr Ala Leu Ser Arg Glu Leu	
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Cys Trp Arg Glu Gly Pro Gly Thr Asp Gln Thr Glu Ala Glu Ala Pro	
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His Thr His Ala Gly Leu Gln Ala Pro Gly Pro Leu Pro Ala Pro Ala	
165 170 175	
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Ala Asp His Leu Leu Thr Ala Ser Trp Gly Ala Asp Pro Val Pro Thr	
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Lys Ala Pro Gly Glu Gly Gln Glu Gly Leu Pro Leu Thr Gly Ala Cys	
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Glu Ala Ala Ala Pro Glu Ser Pro His Gln Ala Glu Pro Tyr Leu Ser	
260 265 270	
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Pro Ser Pro Ser Ala Cys Thr Ala Val Gln Glu Pro Ser Pro Gly Ala	
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Leu Asp Val Thr Ile Met Tyr Lys Gly Arg Thr Val Leu Gln Lys Val	
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gtg gga cac ccg agc tgc acg ttc cta tac ggc ccc cca gac cca gct 960
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 Val Arg Ala Thr Asp Pro Gln Gln Val Ala Phe Pro Ser Pro Ala Glu
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gac acc ccc atc ttc gac ttc aga gtc ttc ttc caa gag ctg gtg gaa 1248
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ttc cgg gca cgg cag cgc cgt ggc tcc cca cgc tat acc atc tac ctg 1296
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acg cag cgt gag ggt gtg tct tcc ctg gat agc agc gac ctc gac ctc 1440
 Thr Gln Arg Glu Gly Val Ser Ser Leu Asp Ser Ser Asp Leu Asp Leu
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tgc ctg tcc agc gcc aac agc ctc tat gac gac atc gag tgc ttc ctt 1488
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<213> Homo sapiens

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 Pro Glu Ala Glu Thr Ala Glu Arg Ala Gly Trp Lys Thr Asn Phe Arg
 85 90 95
 Cys Ala Leu Arg Ser Thr Arg Arg Phe Val Met Leu Arg Asp Asn Ser
 100 105 110
 Gly Asp Pro Ala Asp Pro His Lys Val Tyr Ala Leu Ser Arg Glu Leu
 115 120 125
 Cys Trp Arg Glu Gly Pro Gly Thr Asp Gln Thr Glu Ala Glu Ala Pro
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 Ala Ala Val Pro Pro Pro Gln Gly Gly Pro Pro Gly Pro Phe Leu Ala
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 His Thr His Ala Gly Leu Gln Ala Pro Gly Pro Leu Pro Ala Pro Ala
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 Gly Asp Lys Gly Asp Leu Leu Leu Gln Ala Val Gln Gln Ser Cys Leu
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 Ala Asp His Leu Leu Thr Ala Ser Trp Gly Ala Asp Pro Val Pro Thr
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 Lys Ala Pro Gly Glu Gly Gln Glu Gly Leu Pro Leu Thr Gly Ala Cys
 210 215 220
 Ala Gly Gly Pro Gly Leu Pro Ala Gly Glu Leu Tyr Gly Trp Ala Val
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 Glu Thr Thr Pro Ser Pro Gly Pro Gln Pro Ala Ala Leu Thr Thr Gly
 245 250 255
 Glu Ala Ala Ala Pro Glu Ser Pro His Gln Ala Glu Pro Tyr Leu Ser
 260 265 270
 Pro Ser Pro Ser Ala Cys Thr Ala Val Gln Glu Pro Ser Pro Gly Ala
 275 280 285
 Leu Asp Val Thr Ile Met Tyr Lys Gly Arg Thr Val Leu Gln Lys Val
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 Val Gly His Pro Ser Cys Thr Phe Leu Tyr Gly Pro Pro Asp Pro Ala
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 Val Arg Ala Thr Asp Pro Gln Gln Val Ala Phe Pro Ser Pro Ala Glu
 325 330 335
 Leu Pro Asp Gln Lys Gln Leu Arg Tyr Thr Glu Glu Leu Leu Arg His
 340 345 350
 Val Ala Pro Gly Leu His Leu Glu Leu Arg Gly Pro Gln Leu Trp Ala
 355 360 365
 Arg Arg Met Gly Lys Cys Lys Val Tyr Trp Glu Val Gly Gly Pro Pro
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 Gly Ser Ala Ser Pro Ser Thr Pro Ala Cys Leu Leu Pro Arg Asn Cys
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Asp Thr Pro Ile Phe Asp Phe Arg Val Phe Phe Gln Glu Leu Val Glu
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 Val Leu Val Lys Leu Glu Pro Trp Leu Cys Arg Val His Leu Glu Gly
 450 455 460
 Thr Gln Arg Glu Gly Val Ser Ser Leu Asp Ser Ser Asp Leu Asp Leu
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Trp Leu Leu Gly Glu Ile Ser Ser Gly Cys Tyr Glu Gly Leu Gln Trp	
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ctg gac gag gcc cgc acc tgt ttc cgc gtg ccc tgg aag cac ttc gcg	144
Leu Asp Glu Ala Arg Thr Cys Phe Arg Val Pro Trp Lys His Phe Ala	
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Arg Lys Asp Leu Ser Glu Ala Asp Ala Arg Ile Phe Lys Ala Trp Ala	
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Val Ala Arg Gly Arg Trp Pro Pro Ser Ser Arg Gly Gly Gly Pro Pro	
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Pro Glu Ala Glu Thr Ala Glu Arg Ala Gly Trp Lys Thr Asn Phe Arg	
85 90 95	
tgc gca ctg cgc agc acg cgt cgc ttc gtg atg ctg cgg gat aac tcg	336
Cys Ala Leu Arg Ser Thr Arg Arg Phe Val Met Leu Arg Asp Asn Ser	
100 105 110	

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Gly Asp Pro Ala Asp Pro His Lys Val Tyr Ala Leu Ser Arg Glu Leu	
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Cys Trp Arg Glu Gly Pro Gly Thr Asp Gln Thr Glu Ala Glu Ala Pro	
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Ala Ala Val Pro Pro Pro Gln Gly Gly Pro Pro Gly Pro Phe Leu Ala	
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His Thr His Ala Gly Leu Gln Ala Pro Gly Pro Leu Pro Ala Pro Ala	
165 170 175	
ggt gac aag ggg gac ctc ctg ctc cag gca gtg caa cag agc tgc ctg	576
Gly Asp Lys Gly Asp Leu Leu Leu Gln Ala Val Gln Gln Ser Cys Leu	
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Ala Asp His Leu Leu Thr Ala Ser Trp Gly Ala Asp Pro Val Pro Thr	
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Lys Ala Pro Gly Glu Gly Gln Glu Gly Leu Pro Leu Thr Gly Ala Cys	
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Glu Leu Leu Gly Asn Met Val Leu Ala Pro Leu Pro Asp Pro Gly Pro	
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 Glu Gly Ser Gly Arg Ser Pro Arg Tyr Ala Leu Trp Phe Cys Val Gly
 450 455 460
 gag tca tgg ccc cag gac cag ccg tgg acc aag agg ctc gtg atg gtc 1440
 Glu Ser Trp Pro Gln Asp Gln Pro Trp Thr Lys Arg Leu Val Met Val
 465 470 475 480
 aag gtt gtg ccc acg tgc ctc agg gcc ttg gta gaa atg gcc cgg gta 1488
 Lys Val Val Pro Thr Cys Leu Arg Ala Leu Val Glu Met Ala Arg Val
 485 490 495
 ggg ggt gcc tcc tcc ctg gag aat act gtg gac ctg cac att gac aac 1536
 Gly Gly Ala Ser Ser Leu Glu Asn Thr Val Asp Leu His Ile Asp Asn
 500 505 510
 gac cac cca ctc gac ctc gac gac gac cag tac aag gcc tac ctg cag 1584
 Asp His Pro Leu Asp Leu Asp Asp Asp Gln Tyr Lys Ala Tyr Leu Gln
 515 520 525
 gac ttg gtg gag ggc atg gat ttc cag ggc cct ggg gag agc tga 1629
 Asp Leu Val Glu Gly Met Asp Phe Gln Gly Pro Gly Glu Ser
 530 535 540

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<211> 542

<212> PRT

<213> Homo sapiens

<400> 11

Met Ala Leu Ala Pro Glu Arg Ala Ala Pro Arg Val Leu Phe Gly Glu
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 Trp Leu Leu Gly Glu Ile Ser Ser Gly Cys Tyr Glu Gly Leu Gln Trp
 20 25 30
 Leu Asp Glu Ala Arg Thr Cys Phe Arg Val Pro Trp Lys His Phe Ala
 35 40 45
 Arg Lys Asp Leu Ser Glu Ala Asp Ala Arg Ile Phe Lys Ala Trp Ala
 50 55 60
 Val Ala Arg Gly Arg Trp Pro Pro Ser Ser Arg Gly Gly Gly Pro Pro
 65 70 75 80
 Pro Glu Ala Glu Thr Ala Glu Arg Ala Gly Trp Lys Thr Asn Phe Arg
 85 90 95

T01250" 59644960

[illegible]

THESE

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Glu Ser Trp Pro Gln Asp Gln Pro Trp Thr Lys Arg Leu Val Met Val
465 470 475 480

Lys Val Val Pro Thr Cys Leu Arg Ala Leu Val Glu Met Ala Arg Val
485 490 495

Gly Gly Ala Ser Ser Leu Glu Asn Thr Val Asp Leu His Ile Asp Asn
500 505 510

Asp His Pro Leu Asp Leu Asp Asp Asp Gln Tyr Lys Ala Tyr Leu Gln
515 520 525

Asp Leu Val Glu Gly Met Asp Phe Gln Gly Pro Gly Glu Ser
530 535 540

P011230 59624960

ART 34 AMDT

MDS 2.13

10

cgc tct gcc ctc aac cgc aaa gaa ggg ttg cgt tta gca gag gac cgg 288
 Arg Ser Ala Leu Asn Arg Lys Glu Gly Leu Arg Leu Ala Glu Asp Arg 95

agc aag gac cct cac gac cca cat aaa atc tac gag ttt gtg aac tca 336
 Ser Lys Asp Pro His Asp Pro His Lys Ile Tyr Glu Phe Val Asn Ser 110

gga gtt ggg gac ttt tcc cag cca gac acc tct ccg gac acc aat ggt 384
 Gly Val Gly Asp Phe Ser Gln Pro Asp Thr Ser Pro Asp Thr Asn Gly 115 120 125

gga ggc agt act tct gat acc cag gaa gac att ctg gat gag tta ctg 432
 Gly Gly Ser Thr Ser Asp Thr Gln Glu Asp Ile Leu Asp Glu Leu Leu 130 135 140

ggt aac atg gtg ttg gcc cca ctc cca gat ccg gga ccc cca agc ctg 480
 Gly Asn Met Val Leu Ala Pro Leu Pro Asp Pro Gly Pro Pro Ser Leu 145 150 155 160

gct gta gcc cct gag ccc tgc cct cag ccc ctg ccg agc ccc agc ttg 528
 Ala Val Ala Pro Glu Pro Cys Pro Gln Pro Leu Arg Ser Pro Ser Leu 165 170 175

gac aat ccc act ccc ttc cca aac ctg ggg ccc tct gag aac cca ctg 576
 Asp Asn Pro Thr Pro Phe Pro Asn Leu Gly Pro Ser Glu Asn Pro Leu 180 185 190

aag cgg ctg ttg gtg ccg ggg gaa gag tgg gag ttc gag gtg aca gcc 624
 Lys Arg Leu Leu Val Pro Gly Glu Glu Trp Glu Phe Glu Val Thr Ala 195 200 205

ttc tac cgg ggc cgc caa gtc ttc cag cag acc atc tcc tgc ccg gag 672
 Phe Tyr Arg Gly Arg Gln Val Phe Gln Gln Thr Ile Ser Cys Pro Glu 210 215 220

ggc ctg cgg ctg gtg ggg tcc gaa gtg gga gac agg acg ctg cct gga 720
 Gly Leu Arg Leu Val Gly Ser Glu Val Gly Asp Arg Thr Leu Pro Gly 225 230 235 240

tgg cca gtc aca ctg cca gac cct ggc atg tcc ctg aca gac agg gga 768
 Trp Pro Val Thr Leu Pro Asp Pro Gly Met Ser Leu Thr Asp Arg Gly 245 250 255

gtg atg agc tac gtg agg cat gtg ctg agc tgc ctg ggt ggg gga ctg 816
 Val Met Ser Tyr Val Arg His Val Leu Ser Cys Leu Gly Gly Gly Leu 260 265 270

gct ctc tgg cgg gcc ggg cag tgg ctc tgg gcc cag ccg ctg ggg cac 864
 Ala Leu Trp Arg Ala Gly Gln Trp Leu Trp Ala Gln Arg Leu Gly His 275 280 285

tgc cac aca tac tgg gca gtg agc gag gag ctg ctc ccc aac agc ggg 912
 Cys His Thr Tyr Trp Ala Val Ser Glu Glu Leu Leu Pro Asn Ser Gly 290 295 300

cat ggg cct gat ggc gag gtc ccc aag gac aag gaa gga ggc gtg ttt 960
 His Gly Pro Asp Gly Glu Val Pro Lys Asp Lys Glu Gly Gly Val Phe 305 310 315 320

gac ctg ggg ccc ttc att gta gat ctg att acc ttc acg gaa gga agc 1008
 Asp Leu Gly Pro Phe Ile Val Asp Leu Ile Thr Phe Thr Glu Gly Ser 325 330 335

gga cgc tca cca cgc tat gcc ctc tgg ttc tgt gtg ggg gag tca tgg 1056
 Gly Arg Ser Pro Arg Tyr Ala Leu Trp Phe Cys Val Gly Glu Ser Trp 340 345 350

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ccc cag gac cag ccg tgg acc aag agg ctc gtg atg gtc aag gtt gtg 1104
Pro Gln Asp Gln Pro Trp Thr Lys Arg Leu Val Met Val Lys Val Val
355 360 365

ccc acg tgc ctc agg gcc ttg gta gaa atg gcc cgg gta ggg ggt gcc 1152
Pro Thr Cys Leu Arg Ala Leu Val Glu Met Ala Arg Val Gly Gly Ala
370 375 380

10 tcc tcc ctg gag aat act gtg gac ctg cac att gac aac gac cac cca 1200
Ser Ser Leu Glu Asn Thr Val Asp Leu His Ile Asp Asn Asp His Pro
385 390 395 400

ctc gac ctc gac gac gac cag tac aag gcc tac ctg cag gac ttg gtg 1248
Leu Asp Leu Asp Asp Gln Tyr Lys Ala Tyr Leu Gln Asp Leu Val
405 410 415

gag ggc atg gat ttc cag ggc cct ggg gag agc tga 1284
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<213> Homo sapiens

<400> 2

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Arg Phe Arg Ile Pro Trp Lys His Gly Leu Arg Gln Asp Ala Gln Gln
35 40 45

Glu Asp Phe Gly Ile Phe Gln Ala Trp Ala Glu Ala Thr Gly Ala Tyr
50 55 60

Val Pro Gly Arg Asp Lys Pro Asp Leu Pro Thr Trp Lys Arg Asn Phe
65 70 75 80

40

Arg Ser Ala Leu Asn Arg Lys Glu Gly Leu Arg Leu Ala Glu Asp Arg
85 90 95

Ser Lys Asp Pro His Asp Pro His Lys Ile Tyr Glu Phe Val Asn Ser
100 105 110

Gly Val Gly Asp Phe Ser Gln Pro Asp Thr Ser Pro Asp Thr Asn Gly
115 120 125

50

Gly Gly Ser Thr Ser Asp Thr Gln Glu Asp Ile Leu Asp Glu Leu Leu
130 135 140

Gly Asn Met Val Leu Ala Pro Leu Pro Asp Pro Gly Pro Pro Ser Leu
145 150 155 160

Ala Val Ala Pro Glu Pro Cys Pro Gln Pro Leu Arg Ser Pro Ser Leu
165 170 175

60

Asp Asn Pro Thr Pro Phe Pro Asn Leu Gly Pro Ser Glu Asn Pro Leu
180 185 190

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ART 34 AMDT

10

20

30

40

50

Lys Arg Leu Leu Val Pro Gly Glu Glu Trp Glu Phe Glu Val Thr Ala
195 200 205

Phe Tyr Arg Gly Arg Gln Val Phe Gln Gln Thr Ile Ser Cys Pro Glu
210 215 220

Gly Leu Arg Leu Val Gly Ser Glu Val Gly Asp Arg Thr Leu Pro Gly
225 230 235 240

Trp Pro Val Thr Leu Pro Asp Pro Gly Met Ser Leu Thr Asp Arg Gly
245 250 255

Val Met Ser Tyr Val Arg His Val Leu Ser Cys Leu Gly Gly Gly Leu
260 265 270

Ala Leu Trp Arg Ala Gly Gln Trp Leu Trp Ala Gln Arg Leu Gly His
275 280 285

Cys His Thr Tyr Trp Ala Val Ser Glu Glu Leu Leu Pro Asn Ser Gly
290 295 300

His Gly Pro Asp Gly Glu Val Pro Lys Asp Lys Glu Gly Gly Val Phe
305 310 315 320

Asp Leu Gly Pro Phe Ile Val Asp Leu Ile Thr Phe Thr Glu Gly Ser
325 330 335

Gly Arg Ser Pro Arg Tyr Ala Leu Trp Phe Cys Val Gly Glu Ser Trp
340 345 350

Pro Gln Asp Gln Pro Trp Thr Lys Arg Leu Val Met Val Lys Val Val
355 360 365

Pro Thr Cys Leu Arg Ala Leu Val Glu Met Ala Arg Val Gly Gly Ala
370 375 380

Ser Ser Leu Glu Asn Thr Val Asp Leu His Ile Asp Asn Asp His Pro
385 390 395 400

Leu Asp Leu Asp Asp Asp Gln Tyr Lys Ala Tyr Leu Gln Asp Leu Val
405 410 415

Glu Gly Met Asp Phe Gln Gly Pro Gly Glu Ser
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<212> PRT

<213> Homo sapiens

<400> 3

Ile Ser Asn Ser His Pro Leu Ser Leu Thr Ser Asp Gln
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<210> 4

<211> 4

<212> PRT

<213> Homo sapiens

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444

AMENDED SHEET